LISTING OF THE CLAIMS

33. (NEW) A method for performing allelic differentiation comprising:

acquiring fluorescence intensity data for a plurality of samples wherein the fluorescence intensity data is obtained by amplification of each sample in the presence of at least two fluorophore labels;

generating an angular value for each sample by comparing the fluorescence intensity obtained for the at least two fluorophore labels;

arranging the samples according to their angular value to form an angular-valued based distribution of the samples;

determining a difference value for each sample by taking the difference between the angular value for a selected sample and the angular value for an adjacent sample;

associating at least one difference value range with a selected allelic composition;

evaluating each sample's difference value with respect to the at least one difference value range to determine if the sample resides within the range; and

identifying the allelic composition of each sample on the basis of the difference value range which the sample resides within.

34. (NEW) The method of Claim 33, wherein the allelic compositions comprises a homozygous allele.

35. (NEW) The method of Claim 33, wherein the allelic compositions comprises a heterozygous allele.

36. (NEW) The method of Claim 33, wherein the angular values for each sample are normalized.

37. (NEW) The method of Claim 33, wherein the angular values are calculated as the arctangent between the at least two fluorophore labels.

38. (NEW) The method of Claim 33, further comprising reducing the number of samples undergoing analysis by:

calculating a Euclidean distance for each sample; and

identifying a Euclidean distance threshold for which samples having a Euclidean distance below the threshold are removed from further analysis.

39. (NEW) A method for genotypic analysis comprising:

amplifying a plurality of a genetic samples in the presence of at least two discriminable labels to thereby obtain intensity information indicative of the signals generated by the at least two discriminable labels during amplification;

calculating an angular value for each sample by comparing the intensity information for the at least two discriminable labels used during amplification;

ordering the samples on the basis of their angular value;

calculating a difference value for each sample by taking the difference between the angular value for a selected sample and the angular value for an adjacent sample;

identifying difference value ranges corresponding to homozygous and heterozygous allelic variations; and

determining whether a sample corresponds to a homozygous or heterozygous allelic variant by determining if the sample's difference value resides within the difference value ranges corresponding to homozygous or heterozygous allelic variation.

40. (NEW) The method of Claim 39, wherein the angular values for each sample normalized prior to difference value determination.

41. (NEW) The method of Claim 39, wherein the angular values are calculated as the arctangent between the at least two discriminable labels.